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SEQUENCE LISTING

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Kotin, Robert M.
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<120> AAV5 VECTOR AND USES THEREOF

<130> 14014.0323U3

<140> 09/717,789
<141> 2000-11-21

<150> PCT/US99/11958
<151> 1999-05-28

<150> 60/087,029
<151> 1998-05-28

<160> 24

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 4652
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 1

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gcgaacgcga caggggggag agtgccacac tctcaagcaa gggggttttg taagcagtga 180
tgtcataatg atgtaatgct tattgtcacg cgatagttaa tgattaacag tcatgtgatg 240
tgttttatcc aataggaaga aagcgcgcgt atgagttctc gcgagacttc cggggtataa 300
aagaccgagt gaacgagccc gccgccattc tttgctctgg actgctagag gaccctcgct 360
gccatggcta ccttctatga agtcattgtt cgcgtcccat ttgacgtgga ggaacatctg 420
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tcttccatgg tcctcggccg ctacgtgagt cagattcgcg cccagctggt gaaagtggtc 720
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ttcaacaaga ggaacaccgt ctggctctac ggacccgcca cgaccggcaa gaccaacatc 1380
gcggaggcca tcgcccacac tgtgcccttt tacggctgcg tgaactggac caatgaaaac 1440

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aacaaggtgg ttgaatccgc caaggccatc ctgggggget caaaggtgcg ggtcgatcag    1560
aaatgtaaat cctctgttca aattgattct acccctgtca ttgtaacttc caatacaaac    1620
atgtgtgtgg tggtggatgg gaattccacg acctttgaac accagcagcc gctggaggac    1680
cgcatgttca aatttgaact gactaagcgg ctcccgccag attttggcaa gattactaag    1740
caggaagtca aggacttttt tgcttgggca aaggtcaatc aggtgccggt gactcacgag    1800
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gttcccgaga cgcctcgcag ttcagacgtg actgttgatc ccgctcctct gcgaccgctc    1980
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aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc cgcgaccggc    3960
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<210> 2
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 2

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Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
 1               5                  10                  15
Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
            20                  25                  30
Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
        35                  40                  45
Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
    50                  55                  60
Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
65                  70                  75                  80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
                85                  90                  95
Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
            100                 105                 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115                 120                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140
Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
145                 150                 155                 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175
Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
            180                 185                 190
Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
        195                 200                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
    210                 215                 220
Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225                 230                 235                 240
Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
                245                 250                 255
Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
            260                 265                 270
Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
        275                 280                 285
Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
    290                 295                 300
Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
305                 310                 315                 320
Trp Asn Ser Arg Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp
                325                 330                 335
Asn Ile Ser Asn Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys
            340                 345                 350
Asn Gly Cys Ile Cys His Asn Val Thr His Cys Gln Ile Cys His Gly
        355                 360                 365
Ile Pro Pro Trp Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp
    370                 375                 380
Asp Ala Asn Lys Glu Gln
385                 390
```

<210> 3
<211> 610
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 3

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Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
 1               5                  10                  15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly
            20                  25                  30
Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val
        35                  40                  45
Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
    50                  55                  60
Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
65                  70                  75                  80
Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
                85                  90                  95
Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
            100                 105                 110
Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn
        115                 120                 125
Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
    130                 135                 140
Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145                 150                 155                 160
Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala
                165                 170                 175
Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu
            180                 185                 190
Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala
        195                 200                 205
Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
    210                 215                 220
Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225                 230                 235                 240
Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
                245                 250                 255
Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys Ile Met Ser Leu
            260                 265                 270
Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser Val Pro Glu Asp
        275                 280                 285
Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met Asn Gly Tyr Asp
    290                 295                 300
Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys Gln Arg Ser Phe
305                 310                 315                 320
Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
                325                 330                 335
Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys
            340                 345                 350
Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys
        355                 360                 365
Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn Lys Val Val Glu
    370                 375                 380
```

```
 Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys
 385                 390                 395                 400
 Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val Ile Val Thr Ser
                 405                 410                 415
 Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
             420                 425                 430
 His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys
         435                 440                 445
 Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
     450                 455                 460
 Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
 465                 470                 475                 480
 Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu
                 485                 490                 495
 Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu
             500                 505                 510
 Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp
         515                 520                 525
 Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
     530                 535                 540
 Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp Asn Ile Ser Asn
 545                 550                 555                 560
 Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
                 565                 570                 575
 Cys His Asn Val Thr His Cys Gln Ile Cys His Gly Ile Pro Pro Trp
             580                 585                 590
 Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp Asp Ala Asn Lys
         595                 600                 605
 Glu Gln
     610
```

<210> 4
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 4

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 Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
  1               5                  10                  15
 Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
             20                  25                  30
 Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
         35                  40                  45
 Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
     50                  55                  60
 Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
 65                  70                  75                  80
 Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                 85                  90                  95
 Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
             100                 105                 110
 Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
         115                 120                 125
 Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
     130                 135                 140
```

```
Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160
Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190
Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205
Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220
Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240
Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255
Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270
Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320
Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350
Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365
Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400
Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415
Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430
Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445
Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460
Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480
Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510
Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525
Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560
Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575
Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605
Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620
```

```
Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640
Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655
Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670
Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685
Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700
Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720
Thr Arg Pro Leu
```

<210> 5
<211> 588
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 5

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Thr Ala Pro Thr Gly Lys Arg Ile Asp Asp His Phe Pro Lys Arg Lys
 1                5                  10                  15
Lys Ala Arg Thr Glu Glu Asp Ser Lys Pro Ser Thr Ser Ser Asp Ala
            20                  25                  30
Glu Ala Gly Pro Ser Gly Ser Gln Gln Leu Gln Ile Pro Ala Gln Pro
        35                  40                  45
Ala Ser Ser Leu Gly Ala Asp Thr Met Ser Ala Gly Gly Gly Gly Pro
    50                  55                  60
Leu Gly Asp Asn Asn Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly
65                  70                  75                  80
Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val Thr Lys
                85                  90                  95
Ser Thr Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Gln Tyr Arg
            100                 105                 110
Glu Ile Lys Ser Gly Ser Val Asp Gly Ser Asn Ala Asn Ala Tyr Phe
        115                 120                 125
Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Ser
    130                 135                 140
His Trp Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Tyr Trp Gly
145                 150                 155                 160
Phe Arg Pro Arg Ser Leu Arg Val Lys Ile Phe Asn Ile Gln Val Lys
                165                 170                 175
Glu Val Thr Val Gln Asp Ser Thr Thr Thr Ile Ala Asn Asn Leu Thr
            180                 185                 190
Ser Thr Val Gln Val Phe Thr Asp Asp Asp Tyr Gln Leu Pro Tyr Val
        195                 200                 205
Val Gly Asn Gly Thr Glu Gly Cys Leu Pro Ala Phe Pro Pro Gln Val
    210                 215                 220
Phe Thr Leu Pro Gln Tyr Gly Tyr Ala Thr Leu Asn Arg Asp Asn Thr
225                 230                 235                 240
Glu Asn Pro Thr Glu Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe Pro
                245                 250                 255
Ser Lys Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Thr Tyr Asn Phe
            260                 265                 270
```

```
Glu Glu Val Pro Phe His Ser Ser Phe Ala Pro Ser Gln Asn Leu Phe
        275                 280                 285
Lys Leu Ala Asn Pro Leu Val Asp Gln Tyr Leu Tyr Arg Phe Val Ser
    290                 295                 300
Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly Arg
305                 310                 315                 320
Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg Thr
                325                 330                 335
Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser Ala
            340                 345                 350
Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln Val
        355                 360                 365
Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn Thr
    370                 375                 380
Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn Pro
385                 390                 395                 400
Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser Glu
                405                 410                 415
Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly Gln
            420                 425                 430
Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly Thr
        435                 440                 445
Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg Asp
    450                 455                 460
Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly Ala
465                 470                 475                 480
His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His Pro
                485                 490                 495
Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile Thr
            500                 505                 510
Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser Thr
        515                 520                 525
Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn Ser
    530                 535                 540
Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro
545                 550                 555                 560
Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr Thr
                565                 570                 575
Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
            580                 585
```

<210> 6
<211> 532
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 6

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Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
 1               5                  10                  15
Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
            20                  25                  30
Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
        35                  40                  45
Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
    50                  55                  60
```

```
Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
65                  70                  75                  80
Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
                85                  90                  95
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
            100                 105                 110
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
        115                 120                 125
Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
    130                 135                 140
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
145                 150                 155                 160
Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
                165                 170                 175
Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
            180                 185                 190
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
        195                 200                 205
Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
    210                 215                 220
Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
225                 230                 235                 240
Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
                245                 250                 255
Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
            260                 265                 270
Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
        275                 280                 285
Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
    290                 295                 300
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
305                 310                 315                 320
Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
                325                 330                 335
Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
            340                 345                 350
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
        355                 360                 365
Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
    370                 375                 380
Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
385                 390                 395                 400
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
                405                 410                 415
Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
            420                 425                 430
Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
        435                 440                 445
Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
    450                 455                 460
Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
465                 470                 475                 480
Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
                485                 490                 495
Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
            500                 505                 510
Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
        515                 520                 525
Thr Arg Pro Leu
    530
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<210> 7
<211> 2307
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 7

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ctgcgaccgc tcaattggaa ttcaagtaaa taaagcgagt agtcatgtct tttgttgatc 120
accctccaga ttggttggaa gaagttggtg aaggtcttcg cgagtttttg ggccttgaag 180
cgggcccacc gaaaccaaaa cccaatcagc agcatcaaga tcaagcccgt ggtcttgtgc 240
tgcctggtta taactatctc ggacccggaa acggtctcga tcgaggagag cctgtcaaca 300
gggcagacga ggtcgcgcga gagcacgaca tctcgtacaa cgagcagctt gaggcgggag 360
acaaccccta cctcaagtac aaccacgcgg acgccgagtt tcaggagaag ctcgccgacg 420
acacatcctt cgggggaaac ctcggaaagg cagtctttca ggccaagaaa agggttctcg 480
aacctttgg cctggttgaa gagggtgcta agacggcccc taccggaaag cggatagacg 540
accactttcc aaaaagaaag aaggctcgga ccgaagagga ctccaagcct tccacctcgt 600
cagacgccga agctggaccc agcggatccc agcagctgca aatcccagcc caaccagcct 660
caagtttggg agctgataca atgtctgcgg gaggtggcgg cccattgggc gacaataacc 720
aaggtgccga tggagtgggc aatgcctcgg gagattggca ttgcgattcc acgtggatgg 780
gggacagagt cgtcaccaag tccacccgaa cctgggtgct gcccagctac aacaaccacc 840
agtaccgaga gatcaaaagc ggctccgtcg acggaagcaa cgccaacgcc tactttggat 900
acagcacccc ctgggggtac tttgacttta accgcttcca cagccactgg agcccccgag 960
actggcaaag actcatcaac aactactggg gcttcagacc ccggtccctc agagtcaaaa 1020
tcttcaacat tcaagtcaaa gaggtcacgg tgcaggactc caccaccacc atcgccaaca 1080
acctcacctc caccgtccaa gtgtttacgg acgacgacta ccagctgccc tacgtcgtcg 1140
gcaacgggac cgagggatgc ctgccggcct tccctccgca ggtctttacg ctgccgcagt 1200
acggttacgc gacgctgaac cgcgacaaca cagaaaatcc caccgagagg agcagcttct 1260
tctgcctaga gtactttccc agcaagatgc tgagaacggg caacaacttt gagtttacct 1320
acaactttga ggaggtgccc ttccactcca gcttcgctcc cagtcagaac ctgttcaagc 1380
tggccaaccc gctggtggac cagtacttgt accgcttcgt gagcacaaat aacactggcg 1440
gagtccagtt caacaagaac ctggccggga gatacgccaa cacctacaaa aactggttcc 1500
cggggcccat gggccgaacc cagggctgga acctgggctc cggggtcaac cgcgccagtg 1560
tcagcgcctt cgccacgacc aataggatgg agctcgaggg cgcgagttac caggtgcccc 1620
cgcagccgaa cggcatgacc aacaacctcc agggcagcaa cacctatgcc ctggagaaca 1680
ctatgatctt caacagccag ccggcgaacc cgggcaccac cgccacgtac ctcgagggca 1740
acatgctcat caccagcgag agcgagacgc agccggtgaa ccgcgtggcg tacaacgtcg 1800
gcgggcagat ggccaccaac aaccagagct ccaccactgc ccccgcgacc ggcacgtaca 1860
acctccagga aatcgtgccc ggcagcgtgt ggatggagag ggacgtgtac ctccaaggac 1920
ccatctgggc caagatccca gagacggggg cgcactttca cccctctccg gccatgggcg 1980
gattcggact caaacaccca ccgcccatga tgctcatcaa gaacacgcct gtgcccggaa 2040
atatcaccag cttctcggac gtgcccgtca gcagcttcat cacccagtac agcaccgggc 2100
aggtcaccgt ggagatggag tgggagctca agaaggaaaa ctccaagagg tggaacccag 2160
agatccagta cacaaacaac tacaacgacc cccagtttgt ggactttgcc ccggacagca 2220
ccggggaata cagaaccacc agacctatcg gaacccgata ccttacccga ccccctttaac 2280
ccattcatgt cgcataccct caataaa 2307

<210> 8
<211> 2264
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 8

aggctctcat ttgttcccga gacgcctcgc agttcagacg tgactgttga tcccgctcct 60
ctgcgaccgc tcaattggaa ttcaagattg gttggaagaa gttggtgaag gtcttcgcga 120
gtttttgggc cttgaagcgg gcccaccgaa accaaaaccc aatcagcagc atcaagatca 180
agcccgtggt cttgtgctgc ctggttataa ctatctcgga cccggaaacg gtctcgatcg 240
aggagagcct gtcaacaggg cagacgaggt cgcgcgagag cacgacatct cgtacaacga 300
gcagcttgag gcgggagaca acccctacct caagtacaac cacgcggacg ccgagtttca 360
ggagaagctc gccgacgaca catccttcgg gggaaacctc ggaaaggcag tctttcaggc 420
caagaaaagg gttctcgaac cttttggcct ggttgaagag ggtgctaaga cggcccctac 480
cggaaagcgg atagacgacc actttccaaa aagaaagaag gctcggaccg aagaggactc 540
caagccttcc acctcgtcag acgccgaagc tggacccagc ggatcccagc agctgcaaat 600
cccagcccaa ccagcctcaa gtttgggagc tgatacaatg tctgcgggag gtggcggccc 660
attgggcgac aataaccaag gtgccgatgg agtgggcaat gcctcgggag attggcattg 720
cgattccacg tggatggggg acagagtcgt caccaagtcc acccgaacct gggtgctgcc 780
cagctacaac aaccaccagt accgagagat caaaagcggc tccgtcgacg gaagcaacgc 840
caacgcctac tttggataca gcacccccctg ggggtacttt gactttaacc gcttccacag 900
ccactggagc ccccgagact ggcaaagact catcaacaac tactggggct tcagaccccg 960
gtccctcaga gtcaaaatct tcaacattca agtcaaagag gtcacggtgc aggactccac 1020
caccaccatc gccaacaacc tcacctccac cgtccaagtg tttacggacg acgactacca 1080
gctgccctac gtcgtcggca acgggaccga gggatgcctg ccggccttcc ctccgcaggt 1140
ctttacgctg ccgcagtacg gttacgcgac gctgaaccgc gacaacacag aaaatcccac 1200
cgagaggagc agcttcttct gcctagagta ctttcccagc aagatgctga gaacgggcaa 1260
caactttgag tttacctaca actttgagga ggtgcccttc cactccagct tcgctcccag 1320
tcagaacctg ttcaagctgg ccaacccgct ggtggaccag tacttgtacc gcttcgtgag 1380
cacaaataac actggcggag tccagttcaa caagaacctg gccgggagat acgccaacac 1440
ctacaaaaac tggttcccgg ggcccatggg ccgaacccag ggctggaacc tgggctccgg 1500
ggtcaaccgc gccagtgtca gcgccttcgc cacgaccaat aggatggagc tcgagggcgc 1560
gagttaccag gtgcccccgc agccgaacgg catgaccaac aacctccagg gcagcaacac 1620
ctatgccctg gagaacacta tgatcttcaa cagccagccg gcgaacccgg gcaccaccgc 1680
cacgtacctc gagggcaaca tgctcatcac cagcgagagc gagacgcagc cggtgaaccg 1740
cgtggcgtac aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc 1800
cgcgaccggc acgtacaacc tccaggaaat cgtgcccggc agcgtgtgga tggagaggga 1860
cgtgtacctc caaggaccca tctgggccaa gatcccagag acgggggcgc actttcaccc 1920
ctctccggcc atgggcggat tcggactcaa acacccaccg cccatgatgc tcatcaagaa 1980
cacgcctgtg cccggaaata tcaccagctt ctcggacgtg cccgtcagca gcttcatcac 2040
ccagtacagc accgggcagg tcaccgtgga gatggagtgg gagctcaaga aggaaaactc 2100
caagaggtgg aacccagaga tccagtacac aaacaactac aacgaccccc agtttgtgga 2160
ctttgccccg gacagcaccg gggaatacag aaccaccaga cctatcggaa cccgatacct 2220
tacccgaccc ctttaaccca ttcatgtcgc ataccctcaa taaa 2264

<210> 9
<211> 2264
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 9

aggctctcat ttgttcccga gacgcctcgc agttcagacg tgactgttga tcccgctcct 60
ctgcgaccgc tcaattggaa ttcaagattg gttggaagaa gttggtgaag gtcttcgcga 120
gtttttgggc cttgaagcgg gcccaccgaa accaaaaccc aatcagcagc atcaagatca 180
agcccgtggt cttgtgctgc ctggttataa ctatctcgga cccggaaacg gtctcgatcg 240
aggagagcct gtcaacaggg cagacgaggt cgcgcgagag cacgacatct cgtacaacga 300
gcagcttgag gcgggagaca acccctacct caagtacaac cacgcggacg ccgagtttca 360
ggagaagctc gccgacgaca catccttcgg gggaaacctc ggaaaggcag tctttcaggc 420
caagaaaagg gttctcgaac cttttggcct ggttgaagag ggtgctaaga cggcccctac 480
cggaaagcgg atagacgacc actttccaaa aagaaagaag gctcggaccg aagaggactc 540
caagccttcc acctcgtcag acgccgaagc tggacccagc ggatcccagc agctgcaaat 600
cccagcccaa ccagcctcaa gtttgggagc tgatacaatg tctgcgggag gtggcggccc 660
attgggcgac aataaccaag gtgccgatgg agtgggcaat gcctcgggag attggcattg 720
cgattccacg tggatggggg acagagtcgt caccaagtcc acccgaacct gggtgctgcc 780
cagctacaac aaccaccagt accgagagat caaaagcggc tccgtcgacg gaagcaacgc 840
caacgcctac tttggataca gcaccccctg ggggtacttt gactttaacc gcttccacag 900
ccactggagc ccccgagact ggcaaagact catcaacaac tactggggct tcagaccccg 960
gtccctcaga gtcaaaatct tcaacattca agtcaaagag gtcacggtgc aggactccac 1020
caccaccatc gccaacaacc tcacctccac cgtccaagtg tttacggacg acgactacca 1080
gctgccctac gtcgtcggca acgggaccga gggatgcctg ccggccttcc ctccgcaggt 1140
ctttacgctg ccgcagtacg gttacgcgac gctgaaccgc gacaacacag aaaatcccac 1200
cgagaggagc agcttcttct gcctagagta ctttcccagc aagatgctga gaacgggcaa 1260
caactttgag tttacctaca actttgagga ggtgcccttc cactccagct tcgctcccag 1320
tcagaacctg ttcaagctgg ccaacccgct ggtggaccag tacttgtacc gcttcgtgag 1380
cacaaataac actggcggag tccagttcaa caagaacctg gccgggagat acgccaacac 1440
ctacaaaaac tggttcccgg ggcccatggg ccgaacccag ggctggaacc tgggctccgg 1500
ggtcaaccgc gccagtgtca gcgccttcgc cacgaccaat aggatggagc tcgagggcgc 1560
gagttaccag gtgccccccgc agccgaacgg catgaccaac aacctccagg gcagcaacac 1620
ctatgccctg gagaacacta tgatcttcaa cagccagccg gcgaacccgg gcaccaccgc 1680
cacgtacctc gagggcaaca tgctcatcac cagcgagagc gagacgcagc cggtgaaccg 1740
cgtggcgtac aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc 1800
cgcgaccggc acgtacaacc tccaggaaat cgtgcccggc agcgtgtgga tggagaggga 1860
cgtgtacctc caaggaccca tctgggccaa gatcccagag acgggggcgc actttcaccc 1920
ctctccggcc atgggcggat tcggactcaa acacccaccg cccatgatgc tcatcaagaa 1980
cacgcctgtg cccggaaata tcaccagctt ctcggacgtg cccgtcagca gcttcatcac 2040
ccagtacagc accgggcagg tcaccgtgga gatggagtgg gagctcaaga aggaaaactc 2100
caagaggtgg aacccagaga tccagtacac aaacaactac aacgaccccc agtttgtgga 2160
ctttgccccg gacagcaccg gggaatacag aaccaccaga cctatcggaa cccgatacct 2220
tacccgaccc ctttaaccca ttcatgtcgc ataccctcaa taaa 2264

<210> 10
<211> 1292
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 10

agcgcaaacg gctcgtcgcg cagtttctgg cagaatcctc gcagcgctcg caggaggcgg 60
cttcgcagcg tgagttctcg gctgacccgg tcatcaaaag caagacttcc cagaaataca 120
tggcgctcgt caactggctc gtggagcacg gcatcacttc cgagaagcag tggatccagg 180
aaaatcagga gagctacctc tccttcaact ccaccggcaa ctctcggagc cagatcaagg 240
ccgcgctcga caacgcgacc aaaattatga gtctgacaaa aagcgcggtg gactacctcg 300
tggggagctc cgttcccgag gacatttcaa aaaacagaat ctggcaaatt tttgagatga 360
atggctacga cccggcctac gcgggatcca tcctctacgg ctggtgtcag cgctccttca 420
acaagaggaa caccgtctgg ctctacggac ccgccacgac cggcaagacc aacatcgcgg 480
aggccatcgc ccacactgtg ccctttacg gctgcgtgaa ctggaccaat gaaaactttc 540
cctttaatga ctgtgtggac aaaatgctca tttggtggga ggagggaaag atgaccaaca 600
aggtggttga atccgccaag gccatcctgg ggggctcaaa ggtgcgggtc gatcagaaat 660
gtaaatcctc tgttcaaatt gattctaccc ctgtcattgt aacttccaat acaaacatgt 720
gtgtggtggt ggatgggaat tccacgacct ttgaacacca gcagccgctg gaggaccgca 780
tgttcaaatt tgaactgact aagcggctcc cgccagattt tggcaagatt actaagcagg 840
aagtcaagga ctttttgct tgggcaaagg tcaatcaggt gccggtgact cacgagttta 900
aagttcccag ggaattggcg ggaactaaag gggcggagaa atctctaaaa cgcccactgg 960
gtgacgtcac caatactagc tataaaagtc tggagaagcg ggccaggctc tcatttgttc 1020
ccgagacgcc tcgcagttca gacgtgactg ttgatcccgc tcctctgcga ccgctcaatt 1080
ggaattcaag gtatgattgc aaatgtgact atcatgctca atttgacaac atttctaaca 1140
aatgtgatga atgtgaatat ttgaatcggg gcaaaaatgg atgtatctgt cacaatgtaa 1200
ctcactgtca aatttgtcat gggattcccc cctgggaaaa ggaaaacttg tcagattttg 1260
gggattttga cgatgccaat aaagaacagt aa 1292

<210> 11
<211> 1870
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 11

attctttgct ctggactgct agaggaccct cgctgccatg gctaccttct atgaagtcat 60
tgttcgcgtc ccatttgacg tggaggaaca tctgcctgga atttctgaca gctttgtgga 120
ctgggtaact ggtcaaattt gggagctgcc tccagagtca gatttaaatt tgactctggt 180
tgaacagcct cagttgacgg tggctgatag aattcgccgc gtgttcctgt acgagtggaa 240
caaattttcc aagcaggagt ccaaattctt tgtgcagttt gaaaagggat ctgaatattt 300
tcatctgcac acgcttgtgg agacctccgg catctcttcc atggtcctcg gccgctacgt 360
gagtcagatt cgcgcccagc tggtgaaagt ggtcttccag ggaattgaac cccagatcaa 420
cgactgggtc gccatcacca aggtaaagaa gggcggagcc aataaggtgg tggattctgg 480
gtatattccc gcctacctgc tgccgaaggt ccaaccggag cttcagtggg cgtggacaaa 540
cctggacgag tataaattgg ccgccctgaa tctggaggag cgcaaacggc tcgtcgcgca 600
gtttctggca gaatcctcgc agcgctcgca ggaggcggct tcgcagcgtg agttctcggc 660
tgacccggtc atcaaaagca agacttccca gaaatacatg gcgctcgtca actggctcgt 720
ggagcacggc atcacttccg agaagcagtg gatccaggaa aatcaggaga gctacctctc 780
cttcaactcc accggcaact ctcggagcca gatcaaggcc gcgctcgaca acgcgaccaa 840
aattatgagt ctgacaaaaa gcgcggtgga ctacctcgtg gggagctccg ttcccgagga 900
catttcaaaa aacagaatct ggcaaatttt tgagatgaat ggctacgacc cggcctacgc 960

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gggatccatc ctctacggct ggtgtcagcg ctccttcaac aagaggaaca ccgtctggct    1020
ctacggaccc gccacgaccg gcaagaccaa catcgcggag gccatcgccc acactgtgcc    1080
cttttacggc tgcgtgaact ggaccaatga aaactttccc tttaatgact gtgtggacaa    1140
aatgctcatt tggtgggagg agggaaagat gaccaacaag gtggttgaat ccgccaaggc    1200
catcctgggg ggctcaaagg tgcgggtcga tcagaaatgt aaatcctctg ttcaaattga    1260
ttctaccccc gtcattgtaa cttccaatac aaacatgtgt gtggtggtgg atgggaattc    1320
cacgaccttt gaacaccagc agccgctgga ggaccgcatg ttcaaatttg aactgactaa    1380
gcggctcccg ccagattttg gcaagattac taagcaggaa gtcaaggact tttttgcttg    1440
ggcaaaggtc aatcaggtgc cggtgactca cgagtttaaa gttcccaggg aattggcggg    1500
aactaaaggg gcggagaaat ctctaaaacg cccactgggt gacgtcacca atactagcta    1560
taaaagtctg gagaagcggg ccaggctctc atttgttccc gagacgcctc gcagttcaga    1620
cgtgactgtt gatcccgctc ctctgcgacc gctcaattgg aattcaaggt atgattgcaa    1680
atgtgactat catgctcaat ttgacaacat ttctaacaaa tgtgatgaat gtgaatattt    1740
gaatcggggc aaaaatggat gtatctgtca caatgtaact cactgtcaaa tttgtcatgg    1800
gattcccccc tgggaaaagg aaaacttgtc agattttggg gattttgacg atgccaataa    1860
agaacagtaa                                                          1870
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<210> 12
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 12

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Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
 1               5                  10                  15
Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
            20                  25                  30
Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
        35                  40                  45
Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
    50                  55                  60
Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
65                  70                  75                  80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
                85                  90                  95
Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
            100                 105                 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115                 120                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140
Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
145                 150                 155                 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175
Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
            180                 185                 190
Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
        195                 200                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
    210                 215                 220
Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225                 230                 235                 240
Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
                245                 250                 255
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 Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
            260                 265                 270
 Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
        275                 280                 285
 Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
    290                 295                 300
 Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
 305                 310                 315                 320
 Trp Asn Ser Arg Leu Val Gly Arg Ser Trp
                325                 330
```

<210> 13
<211> 1115
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 13

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 aggagcgcaa acggctcgtc gcgcagtttc tggcagaatc ctcgcagcgc tcgcaggagg      60
 cggcttcgca gcgtgagttc tcggctgacc cggtcatcaa aagcaagact tcccagaaat     120
 acatggcgct cgtcaactgg ctcgtggagc acggcatcac ttccgagaag cagtggatcc     180
 aggaaaatca ggagagctac ctctccttca actccaccgg caactctcgg agccagatca     240
 aggccgcgct cgacaacgcg accaaaatta tgagtctgac aaaaagcgcg gtggactacc     300
 tcgtggggag ctccgttccc gaggacattt caaaaaacag aatctggcaa atttttgaga     360
 tgaatggcta cgacccggcc tacgcgggat ccatcctcta cggctggtgt cagcgctcct     420
 tcaacaagag gaacaccgtc tggctctacg gacccgccac gaccggcaag accaacatcg     480
 cggaggccat cgcccacact gtgcctttt acggctgcgt gaactggacc aatgaaaact     540
 ttccctttaa tgactgtgtg gacaaaatgc tcatttggtg ggaggaggga aagatgacca     600
 acaaggtggt tgaatccgcc aaggccatcc tgggggctc aaaggtgcgg gtcgatcaga     660
 aatgtaaatc ctctgttcaa attgattcta cccctgtcat tgtaacttcc aatacaaaca     720
 tgtgtgtggt ggtggatggg aattccacga cctttgaaca ccagcagccg ctggaggacc     780
 gcatgttcaa atttgaactg actaagcggc tcccgccaga ttttggcaag attactaagc     840
 aggaagtcaa ggacttttt gcttgggcaa aggtcaatca ggtgccggtg actcacgagt     900
 ttaaagttcc cagggaattg gcgggaacta aaggggcgga gaaatctcta aaacgcccac     960
 tgggtgacgt caccaatact agctataaaa gtctggagaa gcgggccagg ctctcatttg    1020
 ttcccgagac gcctcgcagt tcagacgtga ctgttgatcc cgctcctctg cgaccgctca    1080
 attggaattc aagattggtt ggaagaagtt ggtga                               1115
```

<210> 14
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 14

```
 Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
  1               5                  10                  15
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly
            20                  25                  30
 Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val
        35                  40                  45
```

```
Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
    50                  55                  60
Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
65                  70                  75                  80
Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
                85                  90                  95
Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
            100                 105                 110
Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn
        115                 120                 125
Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
    130                 135                 140
Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145                 150                 155                 160
Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala
                165                 170                 175
Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu
            180                 185                 190
Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala
        195                 200                 205
Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
    210                 215                 220
Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225                 230                 235                 240
Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
                245                 250                 255
Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys Ile Met Ser Leu
            260                 265                 270
Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser Val Pro Glu Asp
        275                 280                 285
Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met Asn Gly Tyr Asp
    290                 295                 300
Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys Gln Arg Ser Phe
305                 310                 315                 320
Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
                325                 330                 335
Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys
            340                 345                 350
Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys
        355                 360                 365
Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn Lys Val Val Glu
    370                 375                 380
Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys
385                 390                 395                 400
Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val Ile Val Thr Ser
                405                 410                 415
Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
            420                 425                 430
His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys
        435                 440                 445
Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
    450                 455                 460
Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
465                 470                 475                 480
Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu
                485                 490                 495
Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu
            500                 505                 510
Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp
        515                 520                 525
```

```
Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
    530                 535                 540
Leu Val Gly Arg Ser Trp
545                 550
```

<210> 15
<211> 1690
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 15

```
attctttgct ctggactgct agaggaccct cgctgccatg gctaccttct atgaagtcat      60
tgttcgcgtc ccatttgacg tggaggaaca tctgcctgga atttctgaca gctttgtgga     120
ctgggtaact ggtcaaattt gggagctgcc tccagagtca gatttaaatt tgactctggt     180
tgaacagcct cagttgacgg tggctgatag aattcgccgc gtgttcctgt acgagtggaa     240
caaattttcc aagcaggagt ccaaattctt tgtgcagttt gaaaagggat ctgaatattt     300
tcatctgcac acgcttgtgg agacctccgg catctcttcc atggtcctcg gccgctacgt     360
gagtcagatt cgcgcccagc tggtgaaagt ggtcttccag ggaattgaac cccagatcaa     420
cgactgggtc gccatcacca aggtaaagaa gggcggagcc aataaggtgg tggattctgg     480
gtatattccc gcctacctgc tgccgaaggt ccaaccggag cttcagtggg cgtggacaaa     540
cctggacgag tataaattgg ccgccctgaa tctggaggag cgcaaacggc tcgtcgcgca     600
gtttctggca gaatcctcgc agcgctcgca ggaggcggct tcgcagcgtg agttctcggc     660
tgacccggtc atcaaaagca agacttccca gaaatacatg gcgctcgtca actggctcgt     720
ggagcacggc atcacttccg agaagcagtg gatccaggaa aatcaggaga gctacctctc     780
cttcaactcc accggcaact ctcggagcca gatcaaggcc gcgctcgaca acgcgaccaa     840
aattatgagt ctgacaaaaa gcgcggtgga ctacctcgtg gggagctccg ttcccgagga     900
catttcaaaa aacagaatct ggcaaatttt tgagatgaat ggctacgacc cggcctacgc     960
gggatccatc ctctacggct ggtgtcagcg ctccttcaac aagaggaaca ccgtctggct    1020
ctacggaccc gccacgaccg gcaagaccaa catcgcggag gccatcgccc acactgtgcc    1080
cttttacggc tgcgtgaact ggaccaatga aaactttccc tttaatgact gtgtggacaa    1140
aatgctcatt tggtgggagg agggaaagat gaccaacaag gtggttgaat ccgccaaggc    1200
catcctgggg ggctcaaagg tgcgggtcga tcagaaatgt aaatcctctg ttcaaattga    1260
ttctaccccc gtcattgtaa cttccaatac aaacatgtgt gtggtggtgg atgggaattc    1320
cacgaccttt gaacaccagc agccgctgga ggaccgcatg ttcaaatttg aactgactaa    1380
gcggctcccg ccagattttg gcaagattac taagcaggaa gtcaaggact tttttgcttg    1440
ggcaaaggtc aatcaggtgc cggtgactca cgagtttaaa gttcccaggg aattggcggg    1500
aactaaaggg gcggagaaat ctctaaaacg cccactgggt gacgtcacca atactagcta    1560
taaaagtctg gagaagcggg ccaggctctc atttgttccc gagacgcctc gcagttcaga    1620
cgtgactgtt gatcccgctc ctctgcgacc gctcaattgg aattcaagat tggttggaag    1680
aagttggtga                                                           1690
```

<210> 16
<211> 145
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 16

```
ccatcaccaa ggtaaagaag ggcggagcca ataaggtggt ggattctggg tatattcccg      60
cctacctgct gccgaaggtc caaccggagc ttcagtgggc gtggacaaac ctggacgagt     120
ataaattggc cgccctgaat ctgga                                          145
```

<210> 17
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 17

taagcaggaa gtcaaggact tttttgcttg ggcaaaggtc aatcaggtgc cggtgactca 60
cgagtttaaa gttcccaggg aattggcggg aactaaaggg gcggagaaat ctctaaaacg 120
cccactgggt gacgtcacca atactagcta taaaagtctg gagaagcggg ccag 174

<210> 18
<211> 187
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 18

cactctcaag caaggggttt ttgtaagcag tgatgtcata atgatgtaat gcttattgtc 60
acgcgatagt taatgattaa cagtcatgtg atgtgtttta tccaatagga agaaagcgcg 120
cgtatgagtt ctcgcgagac ttccggggta taaaagaccg agtgaacgag cccgccgcca 180
ttctttg 187

<210> 19
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 19

aaacctcctt gcttgagagt gtggcactct ccccccctgtc gcgttcgctc gctcgctggc 60
tcgtttgggg gggtggcagc tcaaagagct gccagacgac ggcccctctgg ccgtcgcccc 120
cccaaacgag ccagcgagcg agcgaacgcg acaggggggga gagtgcca 168

<210> 20
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 20

aaacctcctt gcttgagagt gtggcactct ccccccctgtc gcgttcgctc gctcgctggc 60
tcgtttgggg gggcgacggc cagagggccg tcgtctgccg gctctttgag ctgccacccc 120
cccaaacgag ccagcgagcg agcgaacgcg acaggggggga gagtgcca 168

<210> 21
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 21
cggtgtga 8

<210> 22
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 22
cggttgag 8

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 23
caaaacctcc ttgcttgaga g 21

<210> 24
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 24

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1               5                  10                  15
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160
Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590
Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```